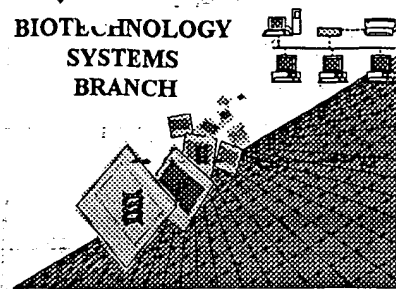


## **RAW SEQUENCE LISTING** **ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/716,964

Source: OIPK

Date Processed by STIC: 12/7/2000

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin30help@uspto.gov](mailto:patin30help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/7/96 964

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid-number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) \_\_\_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10 ☒ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) \_\_\_\_\_ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) \_\_\_\_\_ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/716,964

DATE: 12/07/2000  
 TIME: 07:50:03

Input Set : A:\R10301.app  
 Output Set: N:\CRF3\12072000\I716964.raw

Does Not Comply  
 Corrected Diskette Needed

3 <110> APPLICANT: O'Donnell, Michael E.  
 4 Yurshakov, Alexander  
 5 Yurcheva, Olga  
 6 Jermolami, David  
 7 Bruck, Irina  
 8 Karkhan, John  
 10 <120> TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT  
 11 FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND  
 12 USE THEREOF  
 14 <130> FILE REFERENCE: 22221/1030  
 C--> 16 <140> CURRENT APPLICATION NUMBER: US/09/716,964  
 C--> 17 <141> CURRENT FILING DATE: 2000-11-21  
 19 <150> PRIOR APPLICATION NUMBER: 60/143,202  
 20 <151> PRIOR FILING DATE: 1997-04-08  
 22 <150> PRIOR APPLICATION NUMBER: 08/823,407  
 23 <151> PRIOR FILING DATE: 1997-04-08  
 25 <150> PRIOR APPLICATION NUMBER: 09/057,416  
 26 <151> PRIOR FILING DATE: 1998-04-08  
 28 <160> NUMBER OF SEQ ID NOS: 212  
 30 <170> SOFTWARE: PatentIn Ver. 2.1  
 32 <210> SEQ ID NO: 1  
 33 <211> LENGTH: 2007  
 34 <212> TYPE: DNA  
 35 <213> ORGANISM: Thermus thermophilus  
 37 <400> SEQUENCE: 1  
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 39 gccacctcct ccaggggggc caagggctgc aaggagagga acgtccgcac cagccctat 120  
 40 actagccttg tgaaggccct claccgcgc tlcgcgcgc tcaccttcca ggaggtggtg 180  
 41 gggcaggagc acgtgaagga gccctcctc aaggccatcc gggaggggag gctcgccag 240  
 42 gctactctct tctccgggac caggggcgctg ggaagacca ccacggcgag gctcctcgcc 300  
 43 atggcggggg ggtgcagggg ggaagacccc ccttgcgggg tctgccccca ctgccaggcg 360  
 44 gtgaagaggg ggcgccaccc ggaagtgtg gacattgacg ccgcccagca caactccgtg 420  
 45 gaggacgtgc gggagctgag ggaagagatc cactcgcgc cctctctgc ccccaggaag 480  
 46 gtcttcatcc tggacgaggg ccacatgctc tccaaaagcg ccttcaacgc cctcctcaag 540  
 47 acctggagg ggcgccggcc caacgtctc ttctcttctg ccaccaaccg gcccgagagg 600  
 48 atgcgcccca ccatctctc ccgcaccccg cacttccgct tccgcgcct caccgaggag 660  
 49 gagatgcct ttgaagctag ggcctcctg gaggccgtg ggcgggaggg ggaggaggag 720  
 50 gccctcctcc tcttgcggc cctggcgga cgggccctta gggcgcgga aagcctcctg 780  
 51 gaggccttcc tctcttga aggcgccctc acccggaagg aggtggagcg cgccttaggc 840  
 52 tccccccag ggcgcgggt ggcgcagatc gcgcctccc tgcgagggg gaaaacggcg 900  
 53 gaggccctg gctcgcggc gcgcctctac ggggaagggt acgcgccag gaggctggtc 960  
 54 tggggcctt tggaggtgt ccgggaaggg clctacgcg ccttcggcct cgcgggaacc 1020  
 55 ccccttccc cccgcgccca ggcctgctc gcgcctatg ccgcctgga cggagccatg 1080  
 56 gaggccctc cccgcgcgc cgaagcctta agcctggagg tggccctcct ggaggcggga 1140  
 57 agggccctg ccgcggaggg cctaccccag cccacgggg cctcttccc agaggtcggc 1200  
 58 ccaagccgg aaagccccc gcccccggaa ccccccaggg ccgaggaggg gcccgacctg 1260  
 59 cgggagcggg ggcgggctt cctcgaggcc ctacggccca cctacgggg cctcgtgcgg 1320

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/716,964

DATE: 12/07/2000

TIME: 07:50:03

Input Set : A:\R10301.app

Output Set: N:\CRF3\12072000\I716964.raw

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60 aaggcccgcc cggaggctcc ggaaggccag ctctgectcc ctttccccga aaacaaggcc 1380
61 ttccactacc gcuaggccctc ggaacagaag gtgaagctcc tccccctggc ccaggcccat 1440
62 ttgggqgtgg aggaaggtct cctctctctg gagggaqaaa aaaaaagcct gagcccaagg 1500
63 ccccgcccgq cccacctcc tgaagcgccc gcaccccgq gccctccga gagggaagta 1560
64 gacggcgagg agcggcgga ggaaggcccg gaggagcct tgagacgggt ggtccgctc 1620
65 ctgggggggc ggtgctctg ggtgcgccg cccaggacc ggaagcgcc ggaagaggaa 1680
66 cccctgagcc aagacagat aggggtact ggtatataat ggggcatga cccgaccac 1740
67 cccctcgga caagagacc tggacaacat cctcaagcc ctcgcccga ttgaggcca 1800
68 ggtgcgggg ctcagaga tggtggccga ggcggccc tgcaagagg tctcaccga 1860
69 gatgaccgcc accaagaagg ccattggagg gggggccc ctgactctc aaagttctt 1920
70 gaaegtctgc gccgcccagg tctccgagg caaggtagac ccaagaagg ccgaggagat 1980
71 cggcaccatg ctgaagaact tcattcta 2007
74 <210> SEQ ID NO: 2
75 <211> LENGTH: 529
76 <212> TYPE: PRI
77 <213> ORGANISM: Thermes thermophilus
78 <100> SEQUENCE: 2
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81 1 5 10 15
83 Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
84 20 25 30
86 Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
87 35 40 45
89 Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
90 50 55 60
92 Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
93 65 70 75 80
95 Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
96 85 90 95
98 Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu
99 100 105 110
101 Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser
102 115 120 125
104 Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Gln Pro Pro Pro
105 130 135 140
107 His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro
108 145 150 155 160
110 Thr Ile Leu Ser Arg Thr Glu His Phe Arg Phe Arg Arg Leu Thr Glu
111 165 170 175
113 Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg
114 180 185 190
116 Glu Ala Glu Glu Glu Ala Leu Leu Leu Leu Ala Arg Leu Ala Asp Gly
117 195 200 205
119 Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu
120 210 215 220
122 Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro
123 225 230 235 240
125 Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr
126 245 250 255

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/716,964

DATE: 12/07/2000

TIME: 07:50:03

Input Set : A:\R10301.app

Output Set: N:\CRF3\12072000\I716964.raw

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128 Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala
129          260          265          270
131 Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu
132          275          280          285
134 Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Glu
135          290          295          300
137 Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu
138          305          310          315          320
139 Ala Arg Arg Ser Asp Ala Leu Ser Leu Glu Val Ala Leu Leu Glu Ala
141          325          330          335
143 Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Glu Pro Thr Gly Ala Pro
144          340          345          350
146 Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro
147          355          360          365
149 Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe
150          370          375          380
152 Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg
153          385          390          395          400
155 Pro Glu Val Arg Glu Gly Glu Leu Cys Leu Ala Phe Pro Glu Asp Lys
156          405          410          415
158 Ala Phe His Tyr Arg Lys Ala Ser Glu Glu Cys Val Arg Leu Leu Pro
159          420          425          430
161 Leu Ala Glu Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu
162          435          440          445
164 Gly Glu Lys Lys Ser Leu Ser Pro Arg Pro Arg Pro Ala Pro Pro Pro
165          450          455          460
167 Glu Ala Pro Ala Pro Pro Gly Pro Pro Glu Glu Val Glu Ala Glu
168          465          470          475          480
170 Glu Ala Ala Glu Glu Ala Pro Glu Glu Ala Leu Arg Arg Val Val Arg
171          485          490          495
173 Leu Leu Gly Gly Arg Val Leu Trp Val Arg Arg Pro Arg Thr Arg Glu
174          500          505          510
176 Ala Pro Glu Glu Glu Pro Leu Ser Glu Asp Glu Ile Gly Gly Thr Gly
177          515          520          525
179 Ile
183 <210> SEQ ID NO: 3
184 <211> LENGTH: 1590
185 <212> TYPE: DNA
186 <213> ORGANISM: Thermus thermophilus
188 <400> SEQUENCE: 3
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190 caagtgaaag agccctctct caagggcacc cgggagggga ggtctgcccc ggcctacctc 120
191 ttctccgggc caagggggt ggcaagacc accacggcga ggtctctccc catggcggtg 180
192 gggtagcagg ggaagacccc cccctggcgg gtctgcccc accgacagge ggtgcagagg 240
193 ggcgccacc cggacgttgt ggacattgac gcgcgcagca acaactccgt ggaggacgtg 300
194 cgggagctga gggaaaggat ccacctcgcc cccctctctg cccccaggaa ggtcttcttc 360
195 ctggacgagg ccacatgct ctccaaaagc gccttcacag cctctctcaa gacctggag 420
196 gagccccgc cccagctct ctcgtcttc gccacaccc agcccgagag gatgccccc 480
197 accatctct cccgcacca gaacttcgc ttccgcgcgc tcacggagga ggagatcgcc 540

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/716,964

DATE: 12/07/2000

TIME: 07:50:03

Input Set : A:\R10301.app

Output Set: N:\CRF3\12072000\I716964.raw

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198 ttttaagctcc ggcgcaccc ggaagccctg ggggggagg gggaggagg ggcctctctc 600
199 ctctctgccc gcttgaggga cggggccctt agggagcggg aaagctctct ggaagccttc 660
200 cctctctctg aagcccccct caccgggaag gaggtagagg ggcctctagg ctccccccc 720
201 aggaccgggg tgcgcagat cgcgcctctc ctgcgaggg ggaacaggc ggaagccctg 780
202 ggcctctgccc ggcgcctcta cgggggaggg taacccccga ggaagctggg ctgcgagcctt 840
203 ttggagggtt tccgggaagg cctctacgcc gctttaggcc tggcggggac ccccttccc 900
204 gcccgcgcc cggccctgat cgcgcctat ggcgcctg accgcctg agagagccat ggaagcctc 960
205 gcccgcgct cggagcctt aaactagag gggccctcc tggaggcggg aagggccctg 1020
206 gccgcggagg ccttacccca gcccagggc actccttccc cagaggttcg ccccaagccc 1080
207 gaaagccccc cagcccgagg accccuagg cgcggggagg cgcgcgctt gcggaagcgg 1140
208 tggcgggcct tcttcgagg cctcaggcc accctacggg ccttcgtgca ggaagcccg 1200
209 cggagggtcc ggaagggcca gctctgctc acttcccgg aggaacaggc ctctcactac 1260
210 cgcaggcctt cgaacagaa ggttaggtc ctcccctag cccaggccca ttccgggtg 1320
211 gggagggtcg tctcgtctt gggaggagaa aaaaaagcc tgaagccaa gcccacccc 1380
212 gcccacccc ctgaagccc cgaaccccg ggcctcccg agaggagggt agggcggg 1440
213 gaaacggcgg aagagccccc ggaaggggc ttggggcgg tgcctcgtt cttaagggg 1500
214 cgggtctctt ggttgcggg gcccagggc gggaggggc cggaggaggg acccctgagc 1560
215 ccaaacagga taggggtac tggatataa 1590
216 <210> SEQ ID NO: 4
217 <211> LENGTH: 461
218 <212> TYPE: PRF
219 <213> ORGANISM: Thermus thermophilus
220 <400> SEQUENCE: 4
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222 1 5 10 15
223 Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
224 20 25 30
225 Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
226 35 40 45
227 Lys Thr Thr Thr Ala Arg Leu Ala Met Ala Val Gly Cys Gln Gly
228 50 55 60
229 Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
230 65 70 75 80
231 Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
232 85 90 95
233 Val Glu Asp Val Arg Gln Leu Arg Glu Arg Ile His Leu Ala Pro Leu
234 100 105 110
235 Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Gln Ala His Met Leu Ser
236 115 120 125
237 Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro
238 130 135 140
239 His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Gln Arg Met Pro Pro
240 145 150 155 160
241 Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu
242 165 170 175
243 Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg
244 180 185 190
245 Glu Ala Gln Glu Ala Leu Leu Leu Ala Arg Leu Ala Asp Gly
246 195 200 205

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/716,964

DATE: 12/07/2000

TIME: 07:50:03

Input Set : A:\R10301.app

Output Set: N:\CRF3\12072000\I716964.raw

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203 Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu
204      210      215      220
226 Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro
227 235      240      245      240
268 Gly Phe Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr
269      245      250      255
271 Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala
272      260      265      270
275 Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu
276      275      280      285
278 Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln
279      290      295      300
281 Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu
282 305      310      315      320
294 Ala Arg Arg Ser Asp Ala Leu Ser Leu Glu Val Ala Leu Leu Glu Ala
295      325      330      335
297 Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Gln Pro Thr Gly Ala Pro
298      340      345      350
299 Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro
300      355      360      365
303 Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe
304      370      375      380
306 Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg
307 385      390      395      400
309 Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys
310      405      410      415
312 Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro
313      420      425      430
315 Leu Ala Gln Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu
316      435      440      445
318 Gly Glu Lys Lys Lys Pro Glu Pro Lys Ala Pro Pro Gly Pro Thr Ser
319      450      455      460
319 <210> SEQ ID NO: 5
319 <211> LENGTH: 454
317 <212> TYPE: PRI
318 <213> ORGANISM: Thermus thermophilus
320 <400> SEQUENCE: 5
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322      1      5      10      15
324 Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
325      20      25      30
327 Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
328      35      40      45
330 Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
331      50      55      60
333 Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
334      65      70      75      80
336 Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
337      85      90      95

```

9/7/6, 964

6

<210> 89  
 <211> 182  
 <212> PRT  
 <213> Deinococcus radiodurans

<400> 89

Pro Trp Pro Gln Asp Val Val Val Phe Asp Leu Glu Thr Thr Gly Phe  
 1 5 10 15

Ser Pro Ala Ser Ala Ala Ile Val Glu Ile Gly Ala Val Arg Ile Val  
 20 25 30

Gly Gly Gln Ile Asp Glu Thr Leu Lys Phe Glu Thr Leu Val Arg Pro  
 35 40 45

Thr Arg Pro Asp Gly Ser Met Leu Ser Ile Pro Trp Gln Ala Gln Arg  
 50 55 60

Val His Gly Ile Ser Asp Glu Met Val Arg Arg Ala Pro Ala (Xaa) Lys  
 65 70 75 80

Asp Val Leu Pro Asp Phe Phe Asp Phe Val Asp Gly Ser Ala Val Val  
 85 90 95

Ala His Asn Val Ser Phe Asp Gly Gly Phe Met Arg Ala Gly Ala Glu  
 100 105 110

Arg Leu Gly Leu Ser Trp Ala Pro Glu Arg Glu Leu Cys Thr Met Gln  
 115 120 125

Leu Ser Arg Arg Ala Phe Pro Arg Glu Arg Thr His Asn Leu Thr Val  
 130 135 140

Leu Ala Glu Arg Leu Gly Leu Glu Phe Ala Pro Gly Gly Arg His Arg  
 145 150 155 160

Ser Tyr Gly Asp Val Gln Val Thr Ala Gln Ala Tyr Leu Arg Leu Leu  
 165 170 175

Glu Leu Leu Gly Glu Arg  
 180

all item 10  
 on Enon  
 summary  
 sheet

FYI:

**Please Note:**

Us of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.



VERIFICATION SUMMARY

PATENT APPLICATION: US/09/716,964

DATE: 12/07/2000

TIME: 07:50:04

Input Set : A:\R10301.app

Output Set: N:\CRF3\12072000\I716964.raw

L:16 M:270 C: Current Application Number differs, Replaced Application Number  
 L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:1552 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:17  
 L:1552 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17  
 L:1552 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:17  
 L:1062 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:29  
 L:1062 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:29  
 L:1062 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:29  
 L:1074 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:30  
 L:1074 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:30  
 L:1074 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:30  
 L:1224 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42  
 L:1232 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43  
 L:1506 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:66  
 L:1506 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:66  
 L:1506 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:66  
 L:1519 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:67  
 L:1519 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:67  
 L:1519 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:67  
 L:1532 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:68  
 L:1532 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:68  
 L:1532 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:68  
 L:2169 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:89  
 L:2169 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:89  
 L:2169 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:89  
 L:2169 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:89  
 L:2169 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:89  
 L:2252 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:91  
 L:2252 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:91  
 L:2252 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:91  
 L:2252 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:91  
 L:2252 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:91  
 L:2255 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:91  
 L:2255 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:91  
 L:2255 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:91  
 L:2255 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:91  
 M:340 Repeated in SeqNo=91